RPCIII-14 2089906.s 602250589 602724559 2s10908.r uc21c01.r WHEI755-1

AA16981 2089906.5
BE770745 60225089
BG821160 602224559
AA251869 2810908.7
A1119821 u.c21601.r
BE677859 WHE1755-1
BG744119 602722911
BE76445 210584 MA
BE56445 01342090
AZ286787 RPCI-23-1
AA780606 a156705.8
A57787 601343090
AZ286787 RPCI-23-1
AA780606 a156705.8
BG175072 602336283
BB554828 BB554828
AU05568 AU055686
BH126546 G-1065.1
AW27415 2002002.x
BE426506 WHE0318_H
BW477415 63095 MAR
BE426506 WHE0318_H
BW477415 63095 MAR
BC70200 ST84104.Y
BG742147 602634025
AL325838 TECTROGOD
C70095 C70095 YU11
AV203114 AV2037114 -AV2037114

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 291)
S. Jia., Robey, P., Young, M., Schuler, G., Fowell, J., Yang, L., Lennon, G., Hillier, L., Allen, M., Bowles, L., Geisel, S., Kucaba, T., Marra, Martin, J., Steptoe, M., Tan, F., Theising, B., Bowers, Y., Waylie, T., Waterston, R., Wilson, R., and Francomano, C.

MashD-MGB/NHGRI EST Project
Unpublished (1997)
Contact: Wilson R. / Jia L
WashU-MGB/NHGRI EST Project
WashIngton University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Email: est effeatson, wustl.edu
Email: est effeatson, wustl.edu
Email: est effeatson, wustl.edu
This clone is available royality, free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Sea primer: -40ml3 fwd. Effrom Amersham
High quality sequence stop: 1.

201
Contaction/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ag39d12.sl Jia bone marrow stroma Homo sapiens cDNA clone IMAGE:1119191 3' similar to gb:M31682 INHIBIN BETA B CHAIN PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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CNS058ET
BB428395
                                          AA169881
BF790745
BAA251860
AA251862
A1119821
BE637859
BE7564419
BE756442
BE564287
AZ286787
AA2860606
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AV203714
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BGG01700 FWL_60_CO
BF448402 7N8Bb12.x
AZ256542 RPCI-23.4
BB584200 11H-HA P
BH087207 RPCI-24.3
AI25552 U155h08.y
BF70499 FWL_46_GO
BGG0594747 RHI22_3_DO
BG559747 RHI22_3_BO
                                                                                                                     (without alignments)
786.954 Million cell updates/sec
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                           11351937 segs, 5372889281 residues
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Maximum Match 100%
Listing first 45 summaries
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BES84200
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BG59747
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                                                                           nucleic search, using sw model
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Lennon Marra Wylie

12-MAY-1999

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library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. " 46~\rm g 20~\rm t
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62.0%;
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Unpublished (1997)
                                                                                                                                                                                                                                   Query Match 28.2
Best Local Similarity 62.0
Matches 49; Conservative
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                                                                                                 /... mixed
/dev_stage="mixed"
/lab_host="XL1-Blue MRF'/SOLR"
/lab_host="XL1-Blue MRF'/SOLR"
/note="Wector: pBluescript; Site_1: EcoRI; Site_2: XhoI;
mRNA made from human bone marrow strome, cDNA made by
oligo-dT priming. Directionally cloned. Size-selected for
average insert size >0.5 kb. Library supplied by Dr. Libin
Jia (MGRR). 68 g 59 t
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//db_xref="taxon:12371"
//clone_lib="Fbloral-induced Meristem 1 (FM1)"
//note="Organ: Floral-induced Meristems; Vector:
//note="Organ: Floral-induced meristems" is Site_2:
//note="Organ: Floral-induced in Site_2: Site_2:
//note="Organ: Floral-induced in Site_2: Site_
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Sorghum propinguum.
Sucginum propinguantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Jade; Panitooideae; Andropogoneae; Sorghum.

(Loses 1 to 169)
Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 GAGAGTTCGGAGCTAGGACAAGAGCAAAATCAGGACACACGAAGATCGGCAAGATGGGCAAGATGGTAGAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Botany
The University of Georgia
The University of Georgia
That Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1805
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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FM1_60_C02.91_A003 Floral-Induced Meristem 1 (FM1) Sorghum
propingquum cDNA, mRNA sequence.
BGOS11700 GI:12505705
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Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Indels
      /db_xref="taxon:9606"
/clone="TMAGE:1119191"
/clone_11b="Jia bone marrow stroma"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31.8; DB 10;
Pred. No. 19;
0; Mismatches 27;
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High quality sequence start: 46
High quality sequence stop: 163
PoLYAPYES.
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Best Local Similarity 64.0%;
Matches 48; Conservative
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Locate..., 1310

/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/olone=lib="NCI CGAP_Ov18"
/clone=lib="NCI CGAP_Ov18"
/clone=lib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Christa Prange, The
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.lnl.gov
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: .
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loweryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 310) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF448402 310 bp mRNA EST 01-DEC-2000 7n88b12.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3571558 3' similar to TR:Q9UFIZ Q9UFIZ HYPOTHETICAL 28.7 KD PROTEIN ;, mRNA
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                   15 gcagatcaagatctgcaggaggagggtggttgctactacaagtgcactaaacaggccata 74
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Score 31; DB 11; Length 169;
Pred. No. 29;
0; Mismatches 30; Indels
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Phytophthora solae zoospores. Complementary DNA was synthesized from mRNA using an Xhor-poly(dT) linker-primer. EcorI adapters were ligated to the linker-primer. EcorI adapters were ligated to the blunt-ended cDNA fragments and the products were digested with XhoI for directional cloning into lambda ZAP Express vector. This lambda library was amplified once using E. coli host strain XII Blue MRF, Inserts were then subcloned by mass excision using ExAssist helper phage for conversion into phagemid vector pBK-CMV in E. coli host strain XLOLR. Sequenced using T3 primer: 5' ATT AAC CCT CAC TAA AGG A3'."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="8 d old etiolated hypocotyls 48 h
post-inoculation with Phytophthora sojae zoospores"
/lab_host="E. coli strain XiOLR"
/note="Vector: pBF-CMV; Site_1: EcoRI; Site_2: XhoI; This
cDNA library was constructed from polyA+ enriched mRNA
from etiolated hypocotyls 48 h post-inoculation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Piant hypocotyls infected with Phytophthora sojae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcript obtained from mixed plant-pathogen interaction culture.
                                                                                                                                                                                                                BE584200 517 bp mRNA EST 16-AUG-2000
1-1H-HA PSOjaeHA Glycine max/Phytophthora sojae mixed EST 11brary
CDNA, mRNA sequence.
BE584200
BE584200. GI:9835149
                                                                                                                                                                                                                                                                                                                                            Glycine max/Phytophthora sojae mixed EST library.
Glycine max/Phytophthora sojae mixed EST library
Eukaryota; mixed EST libraries.
1 (bases 1 to 517)
Qutob, D., Hraber, P.T., Sobral, B.W.S. and Gijzen, M.
Comparative analysis of expressed sequences in Phytophthora sojae
Plant Physiol. 123 (1), 243-254 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 ATGGCAGTGTGCAGGAAGACATAGAGTTGCAGAAGGAGCTGAGAGTTCTACATCTTGAGC 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Glycine max/Phytophthora sojae mixed EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strain="Phytophthora sojae race 2 strain P6497"
/cultivar="Glycine max cultivar Harosoy"
/clone_lib=race.135715"
/clone_lib="PsojaeHA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agriculture and Agri-Food Canada
1391 Sandford Street, London, Ontario, Canada NSV
Tel: 519 457 1470
Fax: 519 457 3997
Email: gijzenm@em.agr.ca
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204 CCAAAGAIGC 195
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Mouse BAC End Sequences from Library RPCI-23

AL Onpublished (1999)

Other GSSS: RPCI-23-43915.TV

Contact: Shaying Zhao

Departement of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr.; Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 0208
Email: schaockityr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pleteréde-Jong-med-Duffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
Artom Resea ch Genetics (info@tesgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq Primer: 8P6
Class: RAC ends
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BCORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DHIOB electrocompetent cells (BRL Life Technologies). "
a 124 c 128 g 207 t
                         0;
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RPCI-23-439J15.TJ RPCI-23 Mus musculus genomic clone RPCI-23-439J15
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                            Gaps
                                                                            1 aggiccgigicaggcagaicaagaictgcaggaggaggagggiggigciactacaaagigc 60
                            .
0
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                            Indels
                                                                                                                                                                              61 actaacaggccatactgagctcggcgaggcgaacgtgtcgacggatccgg
                         50;
54.5%; Pred. No. 63; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-439J15"
/clone_lib="RPCI-23"
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                           , DNA sequence.
A2256542
A2256542.1 GI:9460386
Best Local Similarity 54.5
Matches 60; Conservative
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/organism="wistolius"
//strain="C57BL"
/db_xref="laxon:10090"
/clone_ilb="Sugano mouse liver mlia"
/clone_ilb="Sugano mouse liver mlia"
/clone_ilb="Sugano mouse liver mlia"
/clone_ilb="Sugano mouse liver mlia"
/do_stage="adult"

                                                                                                                                                                                        1 (bases I to 945)
Marra,M., Hillier L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                       Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Solurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                        Waterston, R. The Washu-HiMI Mouse EST Project Unpublished (1996)
Contact: Marra M/Mouse EST Project Washu-HiMI Mouse EST Project Washington University School of MedicineP Washington University School of MedicineP A44 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fax: 314 286 1810
Exa: 314 286 1810
Email: mouseestwatson.wustl.edu
This clone is available royalty-free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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BF704949.1 GI:11996610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGT:970691
NGT:970691
Seq primer: custom primer used
High quality sequence stop: 487.
Location/Qualifiers
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/organism≈"Mus musculus"
   AI25552.1 GI:3863077
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                                                                       house mouse.
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                                                                                                BH087207 800 bp DNA GSS 18-JUL-2001
RPCI-24-339C11.TV RPCI-24 Mus musculus genomic clone RPCI-24-339C11
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Thao,S., Mierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvattsbeyn,A., Gebregeorgis,E., Tsegaye,G., Geer,K., Krol,M., Shvattsbeyn,A., Gebregeorgis,E., Mussell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other,GSSs: RPCI-24-33C11.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
Tyll Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPC1-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: schooling.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC epage: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Palate: 339 row: C column: 11
Seg primer: T7
Class: BAC ends.
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/clone="RPCI-24-339C11"
/clone_lib="RPCI-24"
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: PACC
clade: Panicoideae: Andropogoneae: Sorghum.
1 (bases 1 to 506)
Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
TEI: 706 542 1860
Fax: 706 542 1860
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FM1_19_B03.g1_A003 Floral-Induced Meristem 1 (FM1) Sorghum
propinguum cDNA, mRNA sequence.
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An EST database from Sorghum: floral-induced meristems Unpublished (2000)
Contact: Cordonnier-Pratt MM
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High quality sequence start: 10
High quality sequence stop: 390
PoLYAPYES.
                                                                                                                  The University of Georgia
Plant Sciences Building, Rm.
Tel: 706 542 1860
Fax: 706 542 1805
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Contact: Cordonnier-Pratt MM
Department of Botany
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                                                                                      Department of Botany
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 438)

Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                  and Pratt
                                                 Sorghum propinguum
Eukaryocha Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
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-A003 Floral-Induced Meristem 1 (FM1) Sorghum
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Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
TT: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                   1 (bases 1 to 376)
Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C.
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Contact: Cordonnier-Pratt MM
Department of Botany
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Pred. No. 98;
O; Mismatches
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POLYA-Yes.
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propinguum cDNA, mRNA sequence.
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60.8%;
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Matches 48; Conserv
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Gaps

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us-09-486-094-1.rst

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mRNA sequence.
BI159948
BI159948.1 GI:14619949
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                                                                                                                                                                                                                                                                                                                                                                          283 CAGCGCGCCAACCAGCGAA 301
                                                                                                                                                                                                                                                                                                                                    75 ctgagctcggcgaggcgaa 93
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Best Local Similarity 66.7%
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ORIGIN
                                                                                   BASE COUNT
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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1.
BI159948
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                      δŏ
                                                                                                                                                                                                                          /clone_lib="Floral-Induced Meristem 1 (FM1)"
/note="Organ: Floral-Induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_I: XhoI; Site_2:
BCORI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); I 6 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested The
library was made from poly A RNA in the cloning vector
lambda ZAP II. Clones to be sequenced were prepared by
mass excision.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG559747 561 bp mRNA EST 10-APR-2001
RHIZ2_73_B08.q1_A003 Rhizome2 (RHIZ2) Sorghum propinguum cDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Pratt
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sorghum propinguum.
Sorghum propinguum
Sorghum propinguum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 561)
Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 GGACATGAAGAAGTTCAGGAAGATGGCATTTAACAACAACAACAACAGCAGCCAATA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Eax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 gcagatcaagatctgcaggaggagggtggttgctactacaagtgcactaaaggccata 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,L.H.
An EST database from Sorghum: Sorghum propinguum rhizomes Unpublished (2000)
Contact: Cordonnier-Pratt MM
Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29.4; DB 11; Length 506;
Pred. No. 1e+02;
0; Mismatches 31; Indels 0
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/organism="Sorghum propinguum"
/db_xref="texon:132711"
/clone_lib="Rhizome2 (RHIZ2)"
                                                                                                                                                               1. .506
/organism="Sorghum propinguum"
/db_xref="taxon:132711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 14
High quality sequence stop: 561
POLYA-Yes.
                                                                              High quality sequence start: 9
High quality sequence stop: 504
POLYA-No.
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BG559747.1 GI:13588745
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Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 26.7%;
Best Local Similarity 60.8%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 CAGCGCCCAACCAGCGAA 282
                                                            Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 ctgagctcggcgaggcgaa 93
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KEYWORDS
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Authoration Substance of Characteries (Characteries Substance)

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria Primates; Catarrhini; Hominidae, Homo.

E 1 (Dasses 1 to 720)

S NIH-MGC http://mgc.nci.nih.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tassue Procurement: Arc.

CONA Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNI at:

http://mage.llnl.gov

Plate: LLCM1830 row: n column: 24

High quality sequence stop: 712.

High quality sequence stop: 712.
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/db_xref="taxon:9666"
/db_xref="taxon:9666"
/clone="Insex:017043"
/clone="Insex:017043"
/clone=lib="MIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/tab_host="BAR10B (phage_resistant):
/note="Organ: pancreas; Vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dr priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAGG, Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
for average insert size 1.8kb. Library constructed by Ling
for average insert size 1.8kb. Library constructed by Ling
Galifornia, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Supersoript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |
Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
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602863795F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5017943 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                     Query Match 26.7%; Score 29.4; DB 11; Best Local Similarity 60.8%; Pred. No. 1.1e+02; Matches 48; Conservative 0; Mismatches 31;
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Pred. No. 1.1e+02;
0; Mismatches 21;
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ATACCAGGAGACACTGAACTCG 18
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Best Local Similarity 62.2
Matches 46; Conservative
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AQ375775/c
LOCUS
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ORIGIN
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JOURNAL
COMMENT
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                                                                                                                                                             ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                      Homo saplens

Homo saplens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 202)

1 (bases 2 to 202)

1 (bases 2 to 202)

1 (bases 3 to 202)

Najas Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpsoneludatg.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludavig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-GN0497-
130301-003-c02&t3=2001-03-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 200.
Location/Qualifiers
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                                                                                                                                                                                                      BIO57885 202 bp mRNA EST 15-JUN-2001
PM4-GN0497-130301-003-c02 GN0497 Homo sapiens cDNA, mRNA sequence.
BIO57885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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59.8%; Pred. No. 99;
tive 0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="R8N0497"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ctaacaggccatactgagctcg 83
                                                                                                                                                                                                                                                                                BI057885.1 GI:14465415
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Fax: +55-11-2707001
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Best Local Similarity
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VERSION
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SOURCE
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/organism="Homo sapiens"
/db_xref="taxon:966"
/db_xref="taxon:966"
/clone="IMAGE:3688173"
/clone_lib="NuH_MGC_8"
/tissue_type="Burkitt lymphoma"
/tab_nost="DHIOB (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI: Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORIXAhoI sites using the following 5' adaptor: GGACGAGG(G). Size-selected >500bp for average insert size 1:08tb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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PVCI1-148F23.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-148F23,
AQ375775
                                                                                                                                                                                                                             Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1028)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM380 row: o column: 22
BE561966 1028 bp mRNA EST 15-AUG-2000 601347188F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3688173 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29.2; DB 10; Length 1028; Pred. No. 1.4e+02; 0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 47
High quality sequence stop: 675.
Location/Qualifiers
1..1028
                                                            mRNA sequence.
BE561966
BE561966.1 GI:9805686
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 718)

2 hao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter Jose Bac End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Unpublished (1997)

U. Ordact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
Email: bbeqtigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from RACPAC Resources (http://bacpac.med.buffalo.edu.). Clones may be purchased from Research Genetics (info@resgen.com). BAC end search/Dac_end_search.html
Seq primer: SP6
Class: BAC ends.
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1. 718

(Organism="Hono sapiens"

/db_xref="CBB:755659"

/db_xref="CBB:755659"

/db_xref="Taxon:9606"

/db_xref="Taxon:9606"

/db_xref="Taxon:9606"

/dlone="YerCI-11-148F23"

/clone="YerCI-11"

/sex="Male"

/sex="Male"

/coll.type="Lymphocytes"

/coll.type=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: April 2, 2002, 21:04:02 Job time: 8374 sec
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245 GATAACAGG 237
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COMMENT
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AUTHORS
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